

IN THE SPECIFICATION:

Please amend the specification as follows:

On page 1, please replace the paragraph beginning at line 3 with the following paragraph:

This application is a continuation-in-part of U.S. Application Serial No. 09/454,824, filed December 6, 1999, which is a continuation-in-part of U.S. Application Serial No. 09/345,468, filed June 30, 1999, now U.S. Patent No. 6,245,527, the entire disclosure of each is incorporated herein by reference.

On page 13, please replace the paragraph beginning at line 29 with the following paragraph:

FIGURES 1A-1B depict the cDNA sequence of human TANGO 268 (SEQ ID NO:1) and the predicted amino acid sequence of human TANGO 268 (SEQ ID NO:3). The open reading frame of SEQ ID NO:1 extends from nucleotide 36 to nucleotide 1052 of SEQ ID NO:1 (SEQ ID NO:2).

On page 14, please replace the paragraph beginning at line 5 with the following paragraph:

FIGURES 3A-3C depict an alignment of the nucleotide sequence of the open reading frame for human monocyte inhibitory receptor precursor (SEQ ID NO:24; GenBank Accession Number U91928) and the nucleotide sequence of the open reading frame for human TANGO 268 (SEQ ID NO:2). The nucleotide sequences of coding regions of human monocyte inhibitory receptor precursor and human TANGO 268 are 37.7% identical. The nucleotide sequences of full-length, including the 5' and 3' untranslated regions (UTRs), human monocyte inhibitory receptor precursor SEQ ID NO:11; GenBank Accession Number U91928) and human TANGO 268 are 49.9% identical. These alignments were performed using the ALIGN alignment program with a PAM120 scoring matrix, a gap length penalty of 12, and a gap penalty of 4.

On page 14, please replace the paragraph beginning at line 31 with the following paragraph:

FIGURE 6 depicts a cDNA sequence of mouse TANGO 268 (SEQ ID NO:14) and the predicted amino acid sequence of mouse TANGO 268 (SEQ ID NO:16). The open reading frame of SEQ ID NO:14 extends from nucleotide 63 to 1001 of SEQ ID NO:14 (SEQ ID NO:15).

On page 15, please replace the paragraph beginning at line 7 with the following paragraph:

FIGURES 8A-8D depict an alignment of the nucleotide sequence of the open reading frame for human monocyte inhibitory receptor precursor (SEQ ID NO:24; GenBank Accession Number U91928) and the nucleotide sequence of the open reading frame for mouse TANGO 268 (SEQ ID NO:15). The nucleotide sequences of coding regions of human monocyte inhibitory receptor precursor and mouse TANGO 268 are 34.4% identical. The nucleotide sequences of full-length, including the 5' and 3' untranslated regions (UTRs), human monocyte inhibitory receptor precursor SEQ ID NO:11; GenBank Accession Number U91928) and mouse TANGO 268 are 35.6% identical. These alignments were performed using the ALIGN alignment program with a PAM120 scoring matrix, a gap length penalty of 12, and a gap penalty of 4.

On page 23, please replace the paragraph beginning at line 28 with the following paragraph:

A cDNA encoding human TANGO 268 was identified by analyzing the sequences of clones present in a human megakaryocyte cDNA library. This analysis led to the identification of a clone, jthea105e02, encoding full-length human TANGO 268. The human TANGO 268 cDNA of this clone is 2047 nucleotides long (Figures 1A-1B; SEQ ID NO:1). The open reading frame of this cDNA, nucleotides 36 to 1052 of SEQ ID NO:1 (SEQ ID NO:2), encodes a 339 amino acid transmembrane protein (Figures 1A-1B; SEQ ID NO:3) that, as discussed below, represents a platelet-expressed collagen receptor glycoprotein.

On page 26, please replace the paragraph beginning at line 1 with the following paragraph:

Figures 3A-3C shows an alignment of the human TANGO 268 coding region (SEQ ID NO:2) with the human monocyte inhibitory receptor precursor protein coding region (SEQ ID NO:24). The human monocyte inhibitory receptor has been shown to downregulate activation responses by phosphatases. The nucleotide sequences of coding regions of human monocyte inhibitory receptor precursor and human TANGO 268 are 37.7% identical. The full-length nucleic acid sequence of human TANGO 268 (SEQ ID NO:1) exhibits 49.9% identity to the full-length nucleic acid human monocyte inhibitory receptor precursor (SEQ ID NO:11; Accession Number U91928).

On page 29, please replace the paragraph beginning at line 1 with the following paragraph:

In general, mouse TANGO 268 has most homology to various members of the immunoglobulin superfamily that includes NK inhibitory and activating receptors and Fc receptors. The full-length nucleic acid sequence of mouse TANGO 268 exhibits 35.6% identity to the full-length nucleic acid human monocyte inhibitory receptor precursor (SEQ ID NO:11; Accession Number U91928). Figures 8A-8D shows an alignment of the mouse TANGO 268 coding region (SEQ ID NO:15) with the human monocyte inhibitory receptor precursor protein coding region (SEQ ID NO:24). The nucleotide sequences of the coding regions of human monocyte inhibitory receptor precursor and mouse TANGO 268 are 34.4% identical. The nucleotide sequences of the full-length human monocyte inhibitory receptor precursor (SEQ ID NO:11; Accession Number U91928) and full-length mouse TANGO 268 (SEQ ID NO:14) are 35.6% identical. Figure 9 shows that there is an overall 20.3% identity between the mouse TANGO 268 amino acid sequence and the human monocyte inhibitory receptor protein amino acid sequence (SEQ ID NO:12; Accession Number U91928).

On page 34, please replace the paragraph beginning at line 30 with the following paragraph:

Human tissues were studied using Northern blot or RT-PCR analysis. Northern blots (Fig. 14D) revealed no specific message in brain, heart, skeletal muscle, colon, thymus,